

## SEQUENCE LISTING

<110> Madden, Mark  
Weiner, David P.  
Chaplin, Jennifer A.

<120> METHODS FOR PRODUCING ENANTIOMERICALLY PURE  
ALPHA-SUBSTITUTED CARBOXYLIC ACIDS

<130> DIVER1440-2

<140> Not yet known  
<141> 2000-12-28

<150> 60/254,414  
<151> 2000-12-07

<150> 60/173,609  
<151> 1999-12-29

<160> 4

<170> PatentIn Ver. 2.1

<210> 1  
<211> 1041  
<212> DNA  
<213> Unknown Organism

<220>  
<223> Description of Unknown Organism: Obtained from an environmental sample

<220>  
<221> CDS  
<222> (1)..(1041)

<400> 1  
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Met Ser Glu Pro Met Thr Lys Tyr Arg Gly Ala Ala Val Gln Ala Ala  
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ccg gtg ttc ctc gat ctc gac cgc aca gtc gag aaa gcg atc ggc ctg 96  
Pro Val Phe Leu Asp Leu Asp Arg Thr Val Glu Lys Ala Ile Gly Leu  
20 25 30

atc gag cag gcg gcc aag cag gac gtg cgc ctg atc gca ttc cca gag 144  
Ile Glu Gln Ala Ala Lys Gln Asp Val Arg Leu Ile Ala Phe Pro Glu  
35 40 45

act tgg att ccc ggc tat ccc ttt tgg ata tgg ctg ggc gcg ccg gct 192  
Thr Trp Ile Pro Gly Tyr Pro Phe Trp Ile Trp Leu Gly Ala Pro Ala  
50 55 60

tgg ggc atg cgc ttc gtc cag cgc tat ttc gag aat tcg ctc gtg cgc 240  
Trp Gly Met Arg Phe Val Gln Arg Tyr Phe Glu Asn Ser Leu Val Arg  
65 70 75 80

ggc agc aag cag tgg cag gcc ctg gcg gat gcg gcc cgc cgc cac ggc 288  
Gly Ser Lys Gln Trp Gln Ala Leu Ala Asp Ala Ala Arg Arg His Gly  
85 90 95

atg cat gtc gtg gcc ggc tat agc gag cgc gcg ggc ggc agc ctc tat 336  
Met His Val Val Ala Gly Tyr Ser Glu Arg Ala Gly Gly Ser Leu Tyr  
100 105 110

atg ggc cag gcg atc ttc ggc ccc gat ggc gat ctg atc gcc gcg cgc Met Gly Gln Ala Ile Phe Gly Pro Asp Gly Asp Leu Ile Ala Ala Arg	384
115 120 125	
cgc aag ctc aag cct acc cat gcg gag cgc acc gtg ttc ggc gag gga Arg Lys Leu Lys Pro Thr His Ala Glu Arg Thr Val Phe Gly Glu Gly	432
130 135 140	
gac ggc agc cat ctc gcg gtg cac gat acc gcc atc ggg cgc ctc ggc Asp Gly Ser His Leu Ala Val His Asp Thr Ala Ile Gly Arg Leu Gly	480
145 150 155 160	
gcg ctc tgt tgc tgg gag cac atc cag cca ttg tcg aaa tac gcc atg Ala Leu Cys Cys Trp Glu His Ile Gln Pro Leu Ser Lys Tyr Ala Met	528
165 170 175	
tac gcc gcc gac gaa cag gtc cac gtc gcg tcg tgg ccg agc ttc agc Tyr Ala Ala Asp Glu Gln Val His Val Ala Ser Trp Pro Ser Phe Ser	576
180 185 190	
ctc tat cgc ggc atg gcc tat gcg ctc gga ccg gag gtc aat acc gcc Leu Tyr Arg Gly Met Ala Tyr Ala Leu Gly Pro Glu Val Asn Thr Ala	624
195 200 205	
gca agc cag atc tac gcg gtc gag ggc ggc tgc tac gtg ctg gcg tcg Ala Ser Gln Ile Tyr Ala Val Glu Gly Gly Cys Tyr Val Leu Ala Ser	672
210 215 220	
tgc gcg acc gtt tcg ccg gag atg atc aag gta ttg gtg gat acg ccc Cys Ala Thr Val Ser Pro Glu Met Ile Lys Val Leu Val Asp Thr Pro	720
225 230 235 240	
gac aag gag atg ttc ctc aag gcc ggc ggt ttt gcc atg att ttc Asp Lys Glu Met Phe Leu Lys Ala Gly Gly Phe Ala Met Ile Phe	768
245 250 255	
ggg ccc gac ggc cgc gcc ctg gcc gag ccg ctc ccg gag acc gaa gag Gly Pro Asp Gly Arg Ala Leu Ala Glu Pro Leu Pro Glu Thr Glu Glu	816
260 265 270	
gga ctg ctg gtc gcc gat atc gac ctc ggc atg atc gcg ttg gcc aag Gly Leu Leu Val Ala Asp Ile Asp Leu Gly Met Ile Ala Leu Ala Lys	864
275 280 285	
gcg gcg gcc gat ccg gcg cac tat tca cgg ccc gac gta acg cgg Ala Ala Ala Asp Pro Ala Gly His Tyr Ser Arg Pro Asp Val Thr Arg	912
290 295 300	
ctg ctg ctg gat cga cgt ccg gcc caa cgc gtc gtc acg ctt gat gcc Leu Leu Leu Asp Arg Arg Pro Ala Gln Arg Val Val Thr Leu Asp Ala	960
305 310 315 320	
gca ttc gaa ccg caa aac gag gac aag ggc gac gcg ccc gcg ctg cgc Ala Phe Glu Pro Gln Asn Glu Asp Lys Gly Asp Ala Pro Ala Leu Arg	1008
325 330 335	
gtg gtg gcg gaa agc gcc gcc gcg cag tag Val Val Ala Glu Ser Ala Ala Ala Gln	1041
340 345	

<210> 2  
<211> 346  
<212> PRT

<213> Unknown Organism  
<223> Description of Unknown Organism: Obtained from an environmental sample

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Ile Glu Gln Ala Ala Lys Gln Asp Val Arg Leu Ile Ala Phe Pro Glu  
35 40 45  
Thr Trp Ile Pro Gly Tyr Pro Phe Trp Ile Trp Leu Gly Ala Pro Ala  
50 55 60  
Trp Gly Met Arg Phe Val Gln Arg Tyr Phe Glu Asn Ser Leu Val Arg  
65 70 75 80  
Gly Ser Lys Gln Trp Gln Ala Leu Ala Asp Ala Ala Arg Arg His Gly  
85 90 95  
Met His Val Val Ala Gly Tyr Ser Glu Arg Ala Gly Gly Ser Leu Tyr  
100 105 110  
Met Gly Gln Ala Ile Phe Gly Pro Asp Gly Asp Leu Ile Ala Ala Arg  
115 120 125  
Arg Lys Leu Lys Pro Thr His Ala Glu Arg Thr Val Phe Gly Glu Gly  
130 135 140  
Asp Gly Ser His Leu Ala Val His Asp Thr Ala Ile Gly Arg Leu Gly  
145 150 155 160  
Ala Leu Cys Cys Trp Glu His Ile Gln Pro Leu Ser Lys Tyr Ala Met  
165 170 175  
Tyr Ala Ala Asp Glu Gln Val His Val Ala Ser Trp Pro Ser Phe Ser  
180 185 190  
Leu Tyr Arg Gly Met Ala Tyr Ala Leu Gly Pro Glu Val Asn Thr Ala  
195 200 205  
Ala Ser Gln Ile Tyr Ala Val Glu Gly Gly Cys Tyr Val Leu Ala Ser  
210 215 220  
Cys Ala Thr Val Ser Pro Glu Met Ile Lys Val Leu Val Asp Thr Pro  
225 230 235 240  
Asp Lys Glu Met Phe Leu Lys Ala Gly Gly Phe Ala Met Ile Phe  
245 250 255  
Gly Pro Asp Gly Arg Ala Leu Ala Glu Pro Leu Pro Glu Thr Glu Glu  
260 265 270  
Gly Leu Leu Val Ala Asp Ile Asp Leu Gly Met Ile Ala Leu Ala Lys  
275 280 285  
Ala Ala Ala Asp Pro Ala Gly His Tyr Ser Arg Pro Asp Val Thr Arg  
290 295 300  
Leu Leu Leu Asp Arg Arg Pro Ala Gln Arg Val Val Thr Leu Asp Ala  
305 310 315 320  
Ala Phe Glu Pro Gln Asn Glu Asp Lys Gly Asp Ala Pro Ala Leu Arg  
325 330 335  
Val Val Ala Glu Ser Ala Ala Ala Gln  
340 345

<210> 3  
<211> 1014  
<212> DNA  
<213> Unknown Organism  
  
<220>  
<223> Description of Unknown Organism: Obtained from an environmental sample  
  
<220>  
<221> CDS  
<222> (1)..(1014)

Eggplant Database

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atg gat ttg gag gcg acg gtc gac aaa acc att gag ttg atg gaa gaa				96
Met Asp Leu Glu Ala Thr Val Asp Lys Thr Ile Glu Leu Met Glu Glu	20	25	30	
gca gca cgt aat aat gct cgt ctg atc gcc ttt ccg gaa act tgg att				144
Ala Ala Arg Asn Asn Ala Arg Leu Ile Ala Phe Pro Glu Thr Trp Ile	35	40	45	
cca ggc tac cca tgg ttt ctt tgg ctt gac tca cca gca tgg gca atg				192
Pro Gly Tyr Pro Trp Phe Leu Trp Leu Asp Ser Pro Ala Trp Ala Met	50	55	60	
caa ttt gta cgc caa tac cat gag aac tca ttg gag ttg gat ggc cct				240
Gln Phe Val Arg Gln Tyr His Glu Asn Ser Leu Glu Leu Asp Gly Pro	65	70	75	80
caa gct aag cgc att tca gat gca gcc aag cgg ttg gga atc atg gtc				288
Gln Ala Lys Arg Ile Ser Asp Ala Ala Lys Arg Leu Gly Ile Met Val	85	90	95	
acc ctg ggg atg agt gaa cgg gtc ggt ggc acc ctt tac atc agt cag				336
Thr Leu Gly Met Ser Glu Arg Val Gly Gly Thr Leu Tyr Ile Ser Gln	100	105	110	
tgg ttc ata ggc gat aat ggt gac acc att ggg gcc cgg cga aag ttg				384
Trp Phe Ile Gly Asp Asn Gly Asp Thr Ile Gly Ala Arg Arg Lys Leu	115	120	125	
aaa cct act ttt gtt gaa cgt act ttg ttc ggc gaa ggg gat ggt tca				432
Lys Pro Thr Phe Val Glu Arg Thr Leu Phe Gly Glu Gly Asp Gly Ser	130	135	140	
tcg cta gcg gtt ttc gag acg tct gtt gga agg ctg ggt ggc tta tgc				480
Ser Leu Ala Val Phe Glu Thr Ser Val Gly Arg Leu Gly Gly Leu Cys	145	150	155	160
tgt tgg gag cac ctt caa ccg cta aca aaa tac gct ttg tat gca caa				528
Cys Trp Glu His Leu Gln Pro Leu Thr Lys Tyr Ala Leu Tyr Ala Gln	165	170	175	
aat gaa gag att cat tgt gcg gct tgg ccg agc ttt agc ctt tat cct				576
Asn Glu Ile His Cys Ala Ala Trp Pro Ser Phe Ser Leu Tyr Pro	180	185	190	
aat gcg gcg aaa gcc ctg ggg cct gat gtc aat gta gcg gcc tct cga				624
Asn Ala Ala Lys Ala Leu Gly Pro Asp Val Asn Val Ala Ala Ser Arg	195	200	205	
atc tat gcc gtt gaa ggg caa tgc ttc gta cta gcg tcg tgt gcg ctc				672
Ile Tyr Ala Val Glu Gly Gln Cys Phe Val Leu Ala Ser Cys Ala Leu	210	215	220	
gtt tca caa tcc atg atc gat atg ctt tgt aca gat gac gaa aag cat				720
Val Ser Gln Ser Met Ile Asp Met Leu Cys Thr Asp Asp Glu Lys His	225	230	235	240
gcg ttg ctt ctg gct ggt gga cac tca cgt atc ata ggg cct gat				768
Ala Leu Leu Leu Ala Gly Gly His Ser Arg Ile Ile Gly Pro Asp	245	250	255	

ggt ggt gac ttg gtc gcg cct ctt gcc gaa aat gaa gag ggt att ctc	816																																						
Gly Gly Asp Leu Val Ala Pro Leu Ala Glu Asn Glu Glu Gly Ile Leu																																							
260	265	270		tac gca aac ctt gat cct gga gta cgc atc ctt gct aaa atg gcg gca	864	Tyr Ala Asn Leu Asp Pro Gly Val Arg Ile Leu Ala Lys Met Ala Ala		275	280	285		gac cct gct ggt cat tat tcc cgt ccc gac att act cgc ttg cta ata	912	Asp Pro Ala Gly His Tyr Ser Arg Pro Asp Ile Thr Arg Leu Leu Ile		290	295	300		gat cgc agc cct aaa tta ccg gta gtt gaa att gaa ggt gat ctt cgt	960	Asp Arg Ser Pro Lys Leu Pro Val Val Glu Ile Glu Gly Asp Leu Arg		305	310	315	320	cct tac gct ttg ggt aaa gcg tct gag acg ggt gcg caa ctc gaa gaa	1008	Pro Tyr Ala Leu Gly Lys Ala Ser Glu Thr Gly Ala Gln Leu Glu Glu		325	330	335		att tga	1014	Ile	
270																																							
tac gca aac ctt gat cct gga gta cgc atc ctt gct aaa atg gcg gca	864																																						
Tyr Ala Asn Leu Asp Pro Gly Val Arg Ile Leu Ala Lys Met Ala Ala																																							
275	280	285		gac cct gct ggt cat tat tcc cgt ccc gac att act cgc ttg cta ata	912	Asp Pro Ala Gly His Tyr Ser Arg Pro Asp Ile Thr Arg Leu Leu Ile		290	295	300		gat cgc agc cct aaa tta ccg gta gtt gaa att gaa ggt gat ctt cgt	960	Asp Arg Ser Pro Lys Leu Pro Val Val Glu Ile Glu Gly Asp Leu Arg		305	310	315	320	cct tac gct ttg ggt aaa gcg tct gag acg ggt gcg caa ctc gaa gaa	1008	Pro Tyr Ala Leu Gly Lys Ala Ser Glu Thr Gly Ala Gln Leu Glu Glu		325	330	335		att tga	1014	Ile									
285																																							
gac cct gct ggt cat tat tcc cgt ccc gac att act cgc ttg cta ata	912																																						
Asp Pro Ala Gly His Tyr Ser Arg Pro Asp Ile Thr Arg Leu Leu Ile																																							
290	295	300		gat cgc agc cct aaa tta ccg gta gtt gaa att gaa ggt gat ctt cgt	960	Asp Arg Ser Pro Lys Leu Pro Val Val Glu Ile Glu Gly Asp Leu Arg		305	310	315	320	cct tac gct ttg ggt aaa gcg tct gag acg ggt gcg caa ctc gaa gaa	1008	Pro Tyr Ala Leu Gly Lys Ala Ser Glu Thr Gly Ala Gln Leu Glu Glu		325	330	335		att tga	1014	Ile																	
300																																							
gat cgc agc cct aaa tta ccg gta gtt gaa att gaa ggt gat ctt cgt	960																																						
Asp Arg Ser Pro Lys Leu Pro Val Val Glu Ile Glu Gly Asp Leu Arg																																							
305	310	315	320	cct tac gct ttg ggt aaa gcg tct gag acg ggt gcg caa ctc gaa gaa	1008	Pro Tyr Ala Leu Gly Lys Ala Ser Glu Thr Gly Ala Gln Leu Glu Glu		325	330	335		att tga	1014	Ile																									
315	320																																						
cct tac gct ttg ggt aaa gcg tct gag acg ggt gcg caa ctc gaa gaa	1008																																						
Pro Tyr Ala Leu Gly Lys Ala Ser Glu Thr Gly Ala Gln Leu Glu Glu																																							
325	330	335		att tga	1014	Ile																																	
335																																							
att tga	1014																																						
Ile																																							

<210> 4  
<211> 337  
<212> PRT  
<213> Unknown Organism  
<223> Description of Unknown Organism: Obtained from an environmental sample

<400> 4	
Met Lys Glu Ala Ile Lys Val Ala Cys Val Gln Ala Ala Pro Ile Tyr	
1 5 10 15	
Met Asp Leu Glu Ala Thr Val Asp Lys Thr Ile Glu Leu Met Glu Glu	
20 25 30	
Ala Ala Arg Asn Asn Ala Arg Leu Ile Ala Phe Pro Glu Thr Trp Ile	
35 40 45	
Pro Gly Tyr Pro Trp Phe Leu Trp Leu Asp Ser Pro Ala Trp Ala Met	
50 55 60	
Gln Phe Val Arg Gln Tyr His Glu Asn Ser Leu Glu Leu Asp Gly Pro	
65 70 75 80	
Gln Ala Lys Arg Ile Ser Asp Ala Ala Lys Arg Leu Gly Ile Met Val	
85 90 95	
Thr Leu Gly Met Ser Glu Arg Val Gly Gly Thr Leu Tyr Ile Ser Gln	
100 105 110	
Trp Phe Ile Gly Asp Asn Gly Asp Thr Ile Gly Ala Arg Arg Lys Leu	
115 120 125	
Lys Pro Thr Phe Val Glu Arg Thr Leu Phe Gly Glu Gly Asp Gly Ser	
130 135 140	
Ser Leu Ala Val Phe Glu Thr Ser Val Gly Arg Leu Gly Gly Leu Cys	
145 150 155 160	
Cys Trp Glu His Leu Gln Pro Leu Thr Lys Tyr Ala Leu Tyr Ala Gln	
165 170 175	
Asn Glu Glu Ile His Cys Ala Ala Trp Pro Ser Phe Ser Leu Tyr Pro	
180 185 190	
Asn Ala Ala Lys Ala Leu Gly Pro Asp Val Asn Val Ala Ala Ser Arg	
195 200 205	
Ile Tyr Ala Val Glu Gly Gln Cys Phe Val Leu Ala Ser Cys Ala Leu	
210 215 220	
Val Ser Gln Ser Met Ile Asp Met Leu Cys Thr Asp Asp Glu Lys His	
225 230 235 240	
Ala Leu Leu Leu Ala Gly Gly Gly His Ser Arg Ile Ile Gly Pro Asp	
245 250 255	
Gly Gly Asp Leu Val Ala Pro Leu Ala Glu Asn Glu Glu Gly Ile Leu	

260                    265                    270  
Tyr Ala Asn Leu Asp Pro Gly Val Arg Ile Leu Ala Lys Met Ala Ala  
275                    280                    285  
Asp Pro Ala Gly His Tyr Ser Arg Pro Asp Ile Thr Arg Leu Leu Ile  
290                    295                    300  
Asp Arg Ser Pro Lys Leu Pro Val Val Glu Ile Glu Gly Asp Leu Arg  
305                    310                    315                    320  
Pro Tyr Ala Leu Gly Lys Ala Ser Glu Thr Gly Ala Gln Leu Glu Glu  
325                    330                    335  
Ile